

```

11      20      29      38      47      56
5'-TG CAG CAG AGG GAG ACC CGC GGC AAC CCC GGC CTC GGC GTC GCT

65      74      83      92      101      110
GCC ACC ATG ACG GGA AGC AAT ATG TCG GAC GCC TTG GCC AAC GCC GTG TGC CAG
M T G S N M S D A L A N A V C Q

119      128      137      146      155      164
CGC TGC CAG GCC CGC TTC TCC CCC GGC GAG CGC ATT GTC AAC AGC AAT GGC GAG
R C Q A R F S P A E R I V N S N G E

173      182      191      200      209      218
CTG TAC CAT GAG CAC TGC TTC GTG TGT GCC CAG TGC TTC CGG CCC TTC CCC GAG
L Y H E H C F V C A Q C F R P F P E

227      236      245      254      263      272
GGG CTC TTC TAT GAG TTT GAA GGC CGG AAG TAC TGC GAA CAC GAC TTC CAA ATG
G L F Y E F E G R K Y C E H D F Q M

281      290      299      308      317      326
CTG TTT GCT CCG TGC TGT GGA TCC TGC GGT GAG TTC ATC ATC ATT GGC CGC GTC ATC
L F A P C C G S C G E F I I G R V I

335      344      353      362      371      380
AAG GCC ATG AAC AAC TGG CAC CCG GGC TGC TTC CGC TGC GAG CTG TGT GAT
K A M N N N W H P G C F R C E L C D

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FIGURE 1A

[illegible]

**FIGURE 1B**

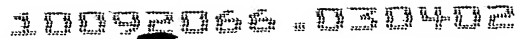
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GGG CAC CGG CAC TAT GAG AAG AAG GGC CTG GCC TAC TGC GAG ACT CAC TAC AAC					
G H R C H Y E K K G L A Y C E T H Y N					
821	830	839	848	857	866
CAG CTC TTC GGG GAC GTC TGC TAC AAC TGC AGC CAT GTG ATT GAA GGC GAT GTG					
Q L F G D V C Y N C S H V I E G D V					
875	884	893	902	911	920
GTG TCG GCC CTC AAC AAG GCC TGG TGT GTG AGC TGC TTC TCC TGC TCC ACC TGC					
V S A L N K A W C V S C F S C S T C					
929	938	947	956	965	974
AAC AGC AAG CTC ACC CTG AAG AAC AAG TTT GTG GAG TTC GAC ATG AAG CCC GTG					
N S K L T L K N K F V E F D M K P V					
983	992	1001	1010	1019	1028
TGT AAG AGG TGC TAC GAG AAG TTC CCG CTG GAG CTG AAG AAG CGG CTG AAG AAG					
C K R C Y E K F P L E L K K R L K K					
1037	1046	1055	1064	1073	1082
CTG TCG GAG CTG ACC TCC CGC AAG GCC CAG CCC AAG GCC ACA GAC CTC AAC TCT					
L S E L T S R K A Q P K A T D L N S					
1091	1100	1109	1118	1127	1136
GCC TGA AGG CCC TCT TGC GCA CTG CCT CTC GGC CCC TCC GCC TTC TCC CCT CCT					
A					

FIGURE 1C

10092000 # 030452

1145	1154	1163	1172	1181	1190
GCT GTC CAT GCT TGG CCC CCT CGT CCC CAT CCA CCT GTG CCC TCC GCA TCT TAC					
1199	1208	1217	1226	1235	1244
CCT CCC TTT CTC TTT CCT CAT TGC CTT CTC CCT TCC TGT TCC CTC ATC TCT GCC					
1253	1262	1271	1280	1289	1298
TTC CCC ATG TCT CTC CTC TCC TTG GCC GTG GCT TCT GTC TGT GAG GAG GCA GGA					
1307	1316	1325	1334	1343	1352
GCT GGG GAG TGG GAG CCT ATG ACC CCA CGT CTG ACA GCC ATG TCC ACC TGT GCC					
1361	1370	1379	1388	1397	1406
CAC AGC TTC CGC CCA CAG ACC TCC AGG GAC AGG AGC AAA TTG CAC CAC AGC TCC					
1415	1424	1433	1442	1451	1460
CCG CCT GGC CTG GCC CTC CCC AGG CGG CTC AGT GGC TCA TGC TGT CCT GTG AGA					
1469	1478	1487	1496	1505	1514
GCC CCT GCC CCA GAG CGG CCC CAC TAA GCG CAT GTG GCT CCT GGG CTA CCC ACA					
1523	1532	1541	1550	1559	1568
GCC AGG GCA GCC TGC TGG AGC CAC AGG GCC AGG GCC ATG CAG ATG GAG GCC TCT					
1577	1586	1595	1604	1613	1622
GGG AGC CAC CTC CAA TCC CTC ACC ACT CAC TCA ACC AGT GGC ACA GTG TCC TTG					
1631	1640	1649	1658	1667	1676
TGC CCA CAC TGA GCC AGC AAG TCC TGC TGT CCA CAC CCA GCT ACC TGG AGG					

FIGURE 1D



1685	1694	1703	1712	1721	1730
GAC AGG ACC CAC CTC CAT CCT TCG GAA GGC CTT CCT GGA ATC CCA CCT TGG CCT					
1739	1748	1757	1766	1775	1784
CCG CCC TCG GTT CCG CCC CGC CCC TCT CCC CCC GAC CTT GGG GCT TGT GTC GAG					
1793	1802	1811	1820	1829	1838
CCC TTG GGT GGG GCC AGG AGG AGG TGA TGG CGT CAG AGG AGG TGT GGT CAG AGG					
1847	1856	1865	1874	1883	1892
TGA CTT GTT CCC ACC TCC AGG GAG GAC GCT TCG TCT TCG GCC AGC GCA GAC CTG					
1901	1910	1919	1928	1937	1946
GTG TTT GTT TGT TTG TTG GGT CAC GCT TGC ACA ATG AAG GCT TGT TCA CAC AAA					
1955					
AAA AAA AAA AAA A 3					

FIGURE 1E

1	M	T	G	S	N	M	S	D	A	L	A	N	A	V	C	Q	R	C	Q	A	R	F	S	P	A	E	R	I	V	N	3540806
1	-	-	-	-	-	M	A	N	A	L	A	S	A	T	C	E	R	C	K	G	G	F	A	P	A	E	K	I	V	N	GI 516012
31	S	N	G	E	L	Y	H	E	H	C	F	V	C	A	Q	C	F	R	P	F	P	E	G	L	F	Y	E	F	E	G	3540806
26	S	N	G	E	L	Y	H	E	Q	C	F	V	C	A	Q	C	F	Q	Q	F	P	E	G	L	F	Y	E	F	E	G	GI 516012
61	R	K	Y	C	E	H	D	F	Q	M	L	F	A	P	C	C	G	S	C	G	E	F	I	I	G	R	V	I	K	A	3540806
56	R	K	Y	C	E	H	D	F	Q	M	L	F	A	P	C	C	H	Q	C	G	E	F	I	I	G	R	V	I	K	A	GI 516012
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86	M	N	N	S	W	H	P	E	C	F	R	C	D	L	C	Q	E	V	L	A	D	I	G	F	V	K	N	A	G	R	GI 516012
121	H	L	C	R	P	C	H	N	R	E	K	A	K	G	L	G	K	Y	I	C	Q	R	C	H	L	V	I	D	E	Q	3540806
116	H	L	C	R	P	C	H	N	R	E	K	A	R	G	L	G	K	Y	I	C	Q	K	C	H	A	I	I	D	E	Q	GI 516012
151	P	L	M	F	R	S	D	A	Y	H	P	D	H	F	N	C	T	H	C	G	K	E	L	T	A	E	A	R	E	L	3540806
146	P	L	I	F	K	N	D	P	Y	H	P	D	H	F	N	C	A	N	C	G	K	E	L	T	A	D	A	R	E	L	GI 516012
181	K	G	E	L	Y	C	L	P	C	H	D	K	M	G	V	P	I	C	G	A	C	R	R	P	I	E	G	R	V	V	3540806
176	K	G	E	L	Y	C	L	P	C	H	D	K	M	G	V	P	I	C	G	A	C	R	R	P	I	E	G	R	V	V	GI 516012
211	N	A	L	G	K	Q	W	H	V	E	H	F	V	C	A	K	C	E	K	P	F	L	G	H	R	H	Y	E	K	K	3540806
206	N	A	M	G	K	Q	W	H	V	E	H	F	V	C	A	K	C	E	K	P	F	L	G	H	R	H	Y	E	R	K	GI 516012
241	G	L	A	Y	C	E	T	H	Y	N	Q	L	F	G	D	V	C	Y	N	C	S	H	V	I	E	G	D	V	V	S	3540806
236	G	L	A	Y	C	E	T	H	Y	N	Q	L	F	G	D	V	C	F	H	C	N	R	V	I	E	G	D	V	V	S	GI 516012

FIGURE 2A

271	A	L	N	K	A	W	C	V	S	C	F	S	C	S	T	C	N	S	K	L	T	L	K	N	K	F	V	E	F	D	3540806
266	A	L	N	K	A	W	C	V	N	C	F	A	C	S	T	C	N	T	K	L	T	L	K	N	K	F	V	E	F	D	GI 516012
301	M	K	P	V	C	K	R	C	Y	E	K	F	P	L	E	L	K	K	R	L	K	K	L	S	E	L	T	S	R	K	3540806
296	M	K	P	V	C	K	K	C	Y	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	S	I	G	GI 516012
331	A	Q	P	K	A	T	D	L	N	S	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3540806
310	A	E	E	K	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 516012

FIGURE 2B

PF-0460-2 CIP

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Guegler, Karl J.  
Corley, Neil C.

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				20					25					30
Ser	Asn	Gly	Glu	Leu	Tyr	His	Glu	His	Cys	Phe	Val	Cys	Ala	Gln
				35					40					45
Cys	Phe	Arg	Pro	Phe	Pro	Glu	Gly	Leu	Phe	Tyr	Glu	Phe	Glu	Gly
				50					55					60
Arg	Lys	Tyr	Cys	Glu	His	Asp	Phe	Gln	Met	Leu	Phe	Ala	Pro	Cys
				65					70					75
Cys	Gly	Ser	Cys	Gly	Glu	Phe	Ile	Ile	Gly	Arg	Val	Ile	Lys	Ala
				80					85					90
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Gly	Lys	Tyr	Ile	Cys	Gln	Arg	Cys	His	Leu	Val	Ile	Asp	Glu	Gln
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Pro	Leu	Met	Phe	Arg	Ser	Asp	Ala	Tyr	His	Pro	Asp	His	Phe	Asn
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Cys	Thr	His	Cys	Gly	Lys	Glu	Leu	Thr	Ala	Glu	Ala	Arg	Glu	Leu
				170					175					180
Lys	Gly	Glu	Leu	Tyr	Cys	Leu	Pro	Cys	His	Asp	Lys	Met	Gly	Val
				185					190					195
Pro	Ile	Cys	Gly	Ala	Cys	Arg	Arg	Pro	Ile	Glu	Gly	Arg	Val	Val
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Asn	Ala	Leu	Gly	Lys	Gln	Trp	His	Val	Glu	His	Phe	Val	Cys	Ala
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Gly Leu Ala Tyr	Cys Glu Thr His Tyr	Asn Gln Leu Phe Gly	Asp		
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Val Cys Tyr Asn	Cys Ser His Val Ile	Glu Gly Asp Val Val	Ser		
	260		265		270
Ala Leu Asn Lys	Ala Trp Cys Val Ser	Cys Phe Ser Cys Ser	Thr		
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Met Lys Pro Val	Cys Lys Arg Cys Tyr	Glu Lys Phe Pro Leu	Glu		
	305		310		315
Leu Lys Lys Arg	Leu Lys Lys Leu Ser	Glu Leu Thr Ser Arg	Lys		
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Tyr	His	Glu	Gln	Cys	Phe	Val	Cys	Ala	Gln	Cys	Phe	Gln	Gln	Phe	40	45	50	55
Pro	Glu	Gly	Leu	Phe	Tyr	Glu	Phe	Glu	Gly	Arg	Lys	Tyr	Cys	Glu	60	65	70	75
His	Asp	Phe	Gln	Met	Leu	Phe	Ala	Pro	Cys	Cys	His	Gln	Cys	Gly	80	85	90	95
Glu	Phe	Ile	Ile	Gly	Arg	Val	Ile	Lys	Ala	Met	Asn	Asn	Ser	Trp	100	105	110	115
His	Pro	Glu	Cys	Phe	Arg	Cys	Asp	Leu	Cys	Gln	Glu	Val	Leu	Ala	120	125	130	135
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Gln	Lys	Cys	His	Ala	Ile	Ile	Asp	Glu	Gln	Pro	Leu	Ile	Phe	Lys	180	185	190	195
Asn	Asp	Pro	Tyr	His	Pro	Asp	His	Phe	Asn	Cys	Ala	Asn	Cys	Gly	200	205	210	215
Lys	Glu	Leu	Thr	Ala	Asp	Ala	Arg	Glu	Leu	Lys	Gly	Glu	Leu	Tyr	220	225	230	235
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Gln	Trp	His	Val	Glu	His	Phe	Val	Cys	Ala	Lys	Cys	Glu	Lys	Pro	280	285	290	295
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